

Amendments to the Specification:

Please replace the paragraph beginning on page 8, line 12, with the following amended paragraph:

Figure 1 illustrates the nucleotide sequence (SEQ ID NO: 1) and predicted amino acid sequence (SEQ ID NO: 2) of rat cortistatin as described in Example 1. The precortistatin cDNA clone displays a 336 nucleotide open reading frame with an N-terminal signal peptide whose cleavage site is indicated by an arrow. The CTG repeat contained within the coding region for the signal peptide is underlined. Two proteolytic cleavage sites (bold KK or KR) could give rise to peptides 13 (hatched lined box) and 14 amino acids long (solid lined box), or to the 29-residue precursor.

Please replace the paragraph beginning on page 8, line 23, with the following amended paragraph:

Figure 2 illustrates the alignment of cortistatin-29 (CST) (SEQ ID NO: 2) and somatostatin-28 (SEQ ID NO: 3) amino acid sequences as described in Example 1.

Please replace the paragraph beginning on page 8, line 26, with the following amended paragraph:

Figure 3 illustrates the nucleotide sequence (SEQ ID NO: 4) and predicted amino acid sequence (SEQ ID NO: 5) of mouse cortistatin as described in Example 1. The precortistatin cDNA clone displays a 327 nucleotide open reading frame with an N-terminal signal peptide whose cleavage site is indicated by an arrow. The CTG repeat contained within the coding region for the signal peptide is underlined. Two proteolytic cleavage sites (KS or KK) could give rise to a 13 amino acid peptide (hatched lined box) and a 14 amino acid peptide (solid lined box).

Please replace the paragraph beginning on page 9, line 3, with the following amended paragraph:

Figure 3a illustrates the alignment of the nucleotide sequence of rat (SEQ ID NO: 1), mouse (SEQ ID NO: 4) and human (SEQ ID NO: 25) preprocortistatin cDNA. The human preprocortistatin cDNA displays a 315 nucleotide open reading frame. The CTG repeat that encodes the amino acid leucine, and that is of variable length between species has been underlined. Two possible polyadenylation signals are marked with an asterisk. Nucleotides conserved among all three species are shown in uppercase, and those not conserved are shown in lowercase.

Please replace the paragraph beginning on page 9, line 13, with the following amended paragraph:

Figure 3b illustrates the alignment of the deduced amino acid sequences of the rat (SEQ ID NO: 2), mouse (SEQ ID NO: 5) and human (SEQ ID NO: 26) cortistatin precursors. The putative dibasic cleavage sites are indicated in bold. Consensus residues are indicated. Proteolytic cleavage sites in human cortistatin (bold RR or RK) could give rise to a 31 amino acid peptide (hatched box), a 29 amino acid peptide, and a 17 amino acid peptide (solid box).